

3D1 heavy chain variable region sequence

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                                30                                60
ATG GGT TGG AAC TGT ATC ATC TTC TTT CTG GTT ACA ACA GCT ACA GGT GTG CAC TCC CAG
M  G  W  N  C  I  I  F  F  L  V  T  T  A  T  G  V  H  S  Q

                                90                                120
GTC CAG CTG CAG CAG TCT GGG CCT GAG CTG GTG AGG CCT GGG GAA TCA GTG AAG ATT TCC
V  Q  L  Q  Q  S  G  P  E  L  V  R  P  G  E  S  V  K  I  S

                                150                                180
TGC AAG GGT TCC GGC TAC ACA TTC ACT GAT TAT GCT ATA CAG TGG GTG AAG CAG AGT CAT
C  K  G  S  G  Y  T  F  T  D  Y  A  I  O  W  V  K  Q  S  H

                                210                                240
GCA AAG AGT CTA GAG TGG ATT GGA GTT ATT AAT ATT TAC TAT GAT AAT ACA AAC TAC AAC
A  K  S  L  E  W  I  G  V  I  N  I  Y  Y  D  N  T  N  Y  N

                                270                                300
CAG AAG TTT AAG GGC AAG GCC ACA ATG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAT ATG
O  K  F  K  G  K  A  T  M  T  V  D  K  S  S  S  T  A  Y  M

                                330                                360
GAA CTT GCC AGA TTG ACA TCT GAG GAT TCT GCC ATC TAT TAC TGT GCA AGA GCG GCC TGG
E  L  A  R  L  T  S  E  D  S  A  I  Y  Y  C  A  R  A  A  W

                                390
TAT ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
Y  M  D  Y  W  G  Q  G  T  S  V  T  V  S  S

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002270" 9582960

Figure 1 (A)

3D1 light chain variable region sequence

30 60
 ATG GAT TCA CAG GCC CAG GTT CTT ATA TTG CTG CTG CTA TGG GTA TCT GGT ACC TGT GGG
 M D S Q A Q V L I L L L L W V S G T C G

90 120
 GAC ATT GTG CTG TCA CAG TCT CCA TCC TCC CTG GCT GTG TCA GCA GGA GAG AAG GTC ACT
 D I V L S Q S P S S L A V S A G E K V T

150 180
 ATG AGC TGC AAA TCC AGT CAG AGT CTG CTC AAC AGT AGA ACC CGA GAG AAC TAC TTG GCT
 M S C K S S Q S L L N S R T R E N Y L A

210 240
 TGG TAC CAG CAG AAA CCA GGG CAG TCT CCT AAA CTG CTG ATC TAC TGG GCA TCC ACT AGG
 W Y Q Q K P G Q S P K L L I Y W A S T R

270 300
 GAA TCT GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC
 E S G V P D R F T G S G S G T D F T L T

330 360
 ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA GTT TAT TAC TGC ACG CAA TCT TAT AAT CTT
 I S S V Q A E D L A V Y Y C T O S Y N L

390
 TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA
 Y T F G G G T K L E I K

00220-962700

Figure 1 (B)

Hu3D1 heavy chain variable region sequence

30 60
 ATG GGT TGG AAC TGT ATC ATC TTC TTT CTG GTT ACC ACA GCT ACA GGT GTG CAC TCC CAG
 M G W N C I I F F L V T T A T G V H S Q

90 120
 GTC CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG CCT GGG AGC TCA GTG AAG GTG TCC
 V Q L V Q S G A E V K K P G S S V K V S

150 180
 TGG AAA GCT TCC GGC TAC ACA TTC ACT GAT TAT GCT ATA CAG TGG GTG AGA CAG GCT CCT
 C K A S G Y T F T D Y A I Q W V R Q A P

210 240
 - GGA CAG GGC CTC GAG TGG ATT GGA GTT ATT AAT ATT TAC TAT GAT AAT ACA AAC TAC AAC
 G Q G L E W I G V I N I Y Y D N T N Y N

270 300
 CAG AAG TTT AAG GGC AAG GCC ACA ATG ACT GTA GAC AAG TCG ACG AGC ACA GCC TAT ATG
Q K F K G K A T M T V D K S T S T A Y M

330 360
 GAA CTT AGT TCT TTG AGA TCT GAG GAT ACG GCC GTT TAT TAC TGT GCA AGA GCG GCC TGG
 E L S S L R S E D T A V Y Y C A R A A W

390
 TAT ATG GAC TAC TGG GGT CAA GGT ACC CTT GTC ACC GTC TCC TCA
Y M D Y W G Q G T L V T V S S

0022700
 072700
 962700
 0962700

Figure 2 (A)

Hu3D1 light chain variable region sequence

30 60
 ATG GAT TCA CAG GCC CAG GTT CTT ATA TTG CTG CTG CTA TGG GTA TCT GGC ACC TGT GGG
 M D S Q A Q V L I L L L L W V S G T C G

90 120
 GAC ATT GTG CTG ACA CAG TCT CCA GAT TCC CTG GCT GTA AGC TTA GGA GAG AGG GCC ACT
D I V L T Q S P D S L A V S L G E R A T

150 180
 ATT AGC TGC AAA TCC AGT CAG AGT CTG CTC AAC AGT AGA ACC CGA GAG AAC TAC TTG GCT
 I S C K S S O S L L N S R T R E N Y L A

210 240
 TGG TAC CAG CAG AAA CCA GGG CAG CCT CCT AAA CTG CTG ATC TAC TGG GCA TCC ACT AGG
 W Y Q Q K P G Q P P K L L I Y W A S T R

270 300
 GAA TCT GGG GTC CCT GAT CGC TTC AGT GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC
E S G V P D R F S G S G S G T D F T L T

330 360
 ATC AGC AGT CTG CAG GCT GAA GAC GTG GCA GTT TAT TAC TGC ACG CAA TCT TAT AAT CTT
 I S S L Q A E D V A V Y Y C T O S Y N L

390
 TAC ACG TTC GGA CAG GGG ACC AAG GTG GAA ATA AAA
Y T F G Q G T K V E I K

Figure 2 (B)

00220" 96842960

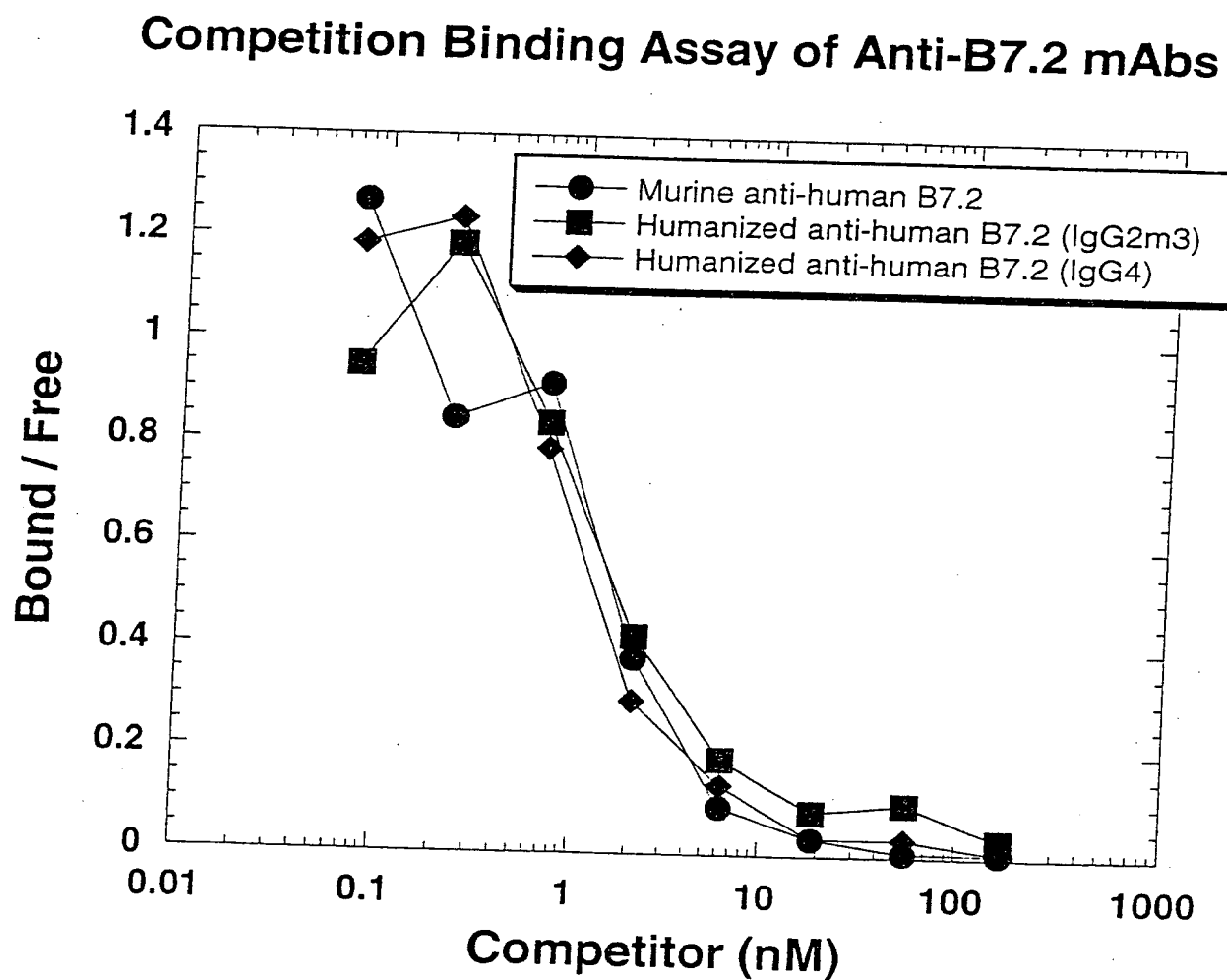


Figure 3

Direct Binding Assay of Anti-B7.2 mAbs

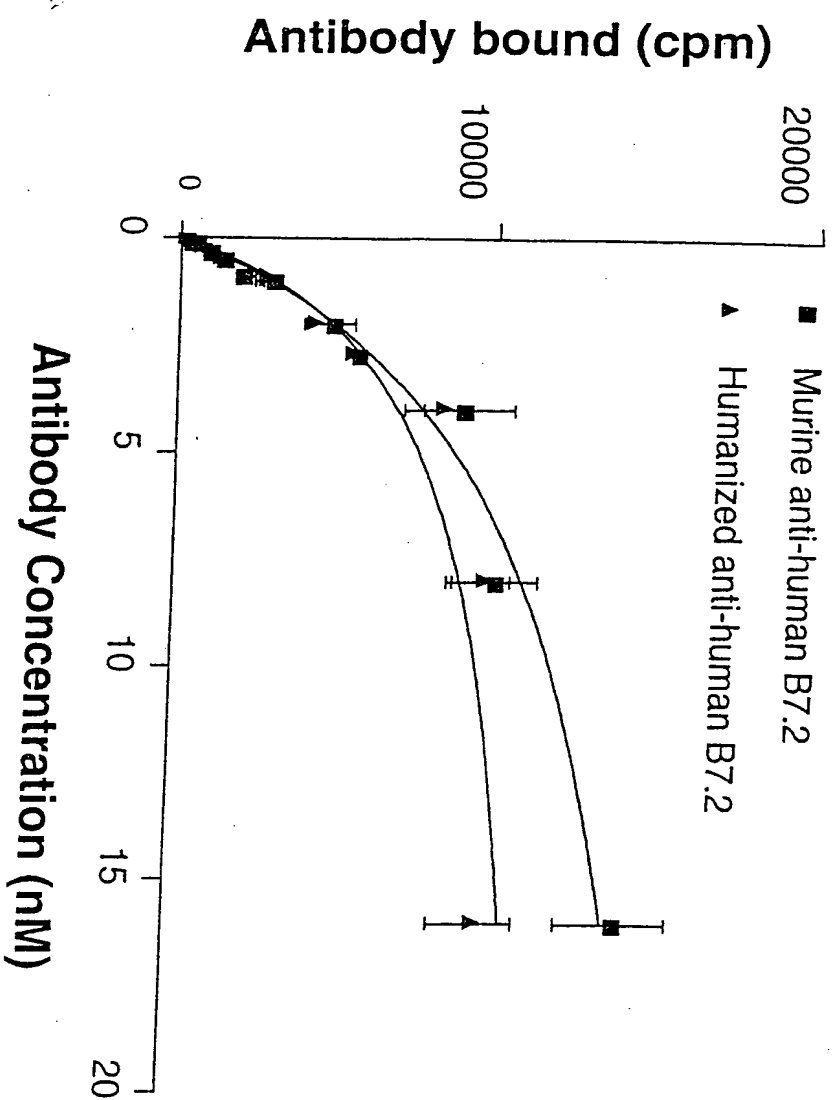


Figure 4

09627896.072700

002220" 96822960

Inhibition of CD28⁺ T Cell Proliferation by Anti-B7.2 mAbs

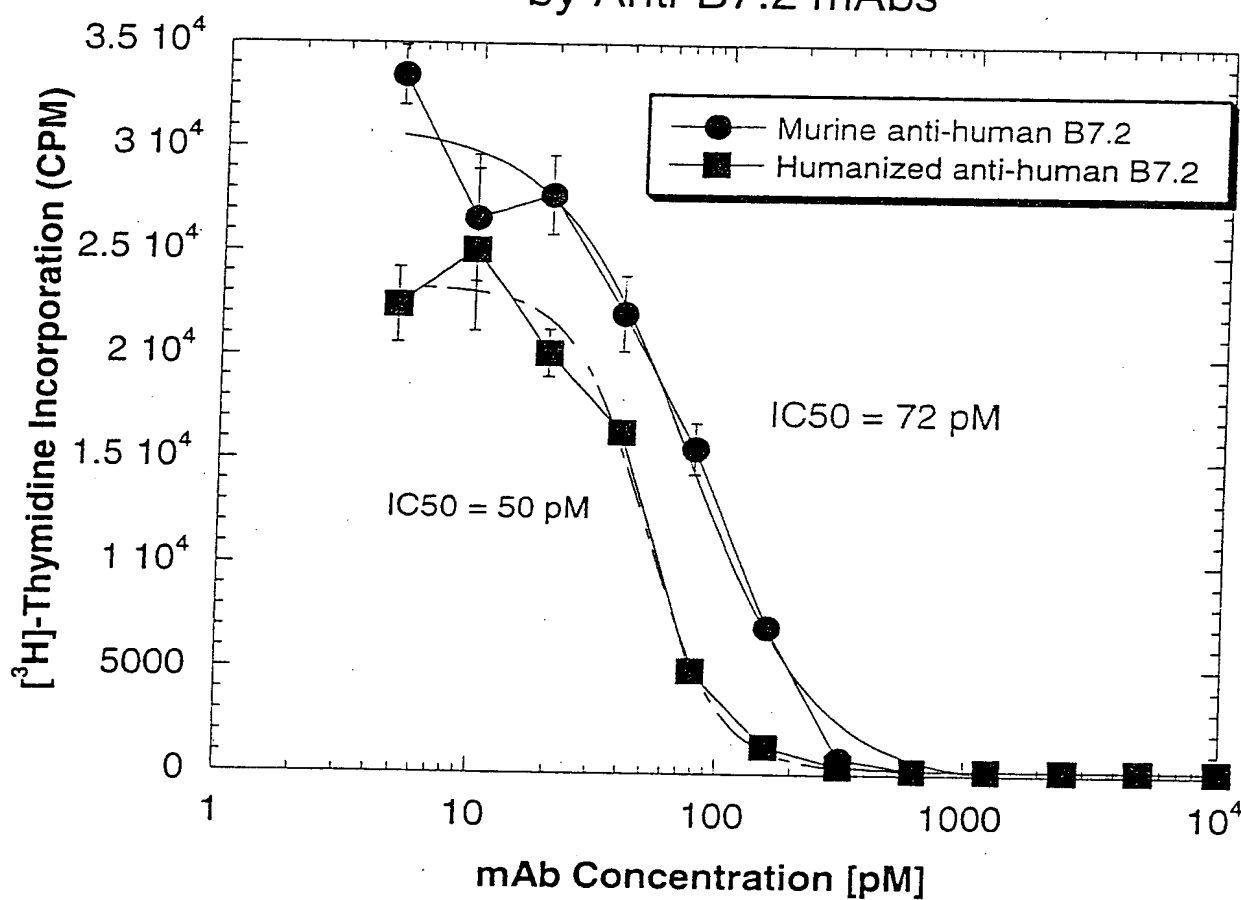


Figure 5

Inhibition of a Mixed Lymphocyte Reaction by Anti-B7 Antibodies and CTLA4Ig

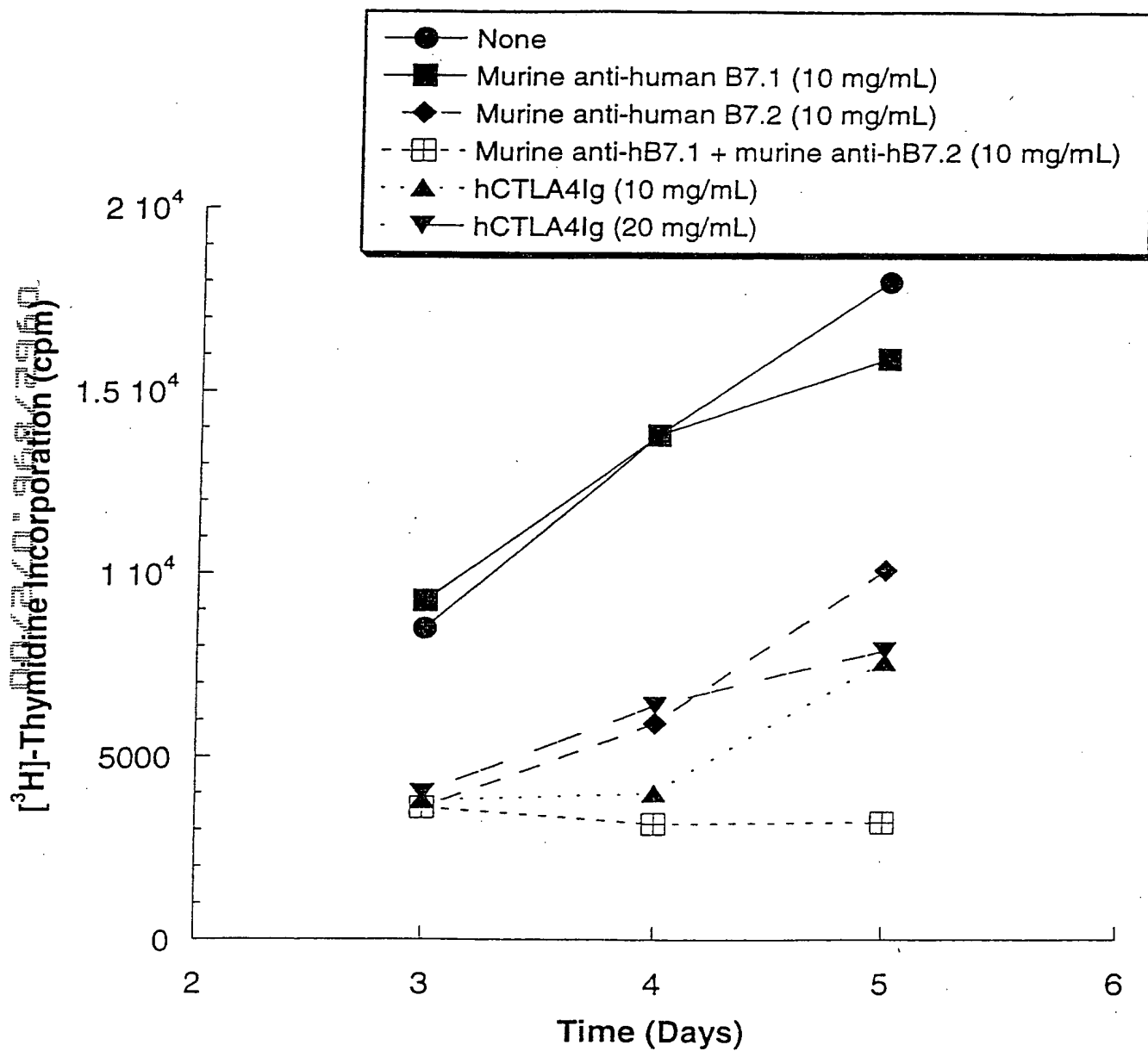


Figure 6

002240" 96822960

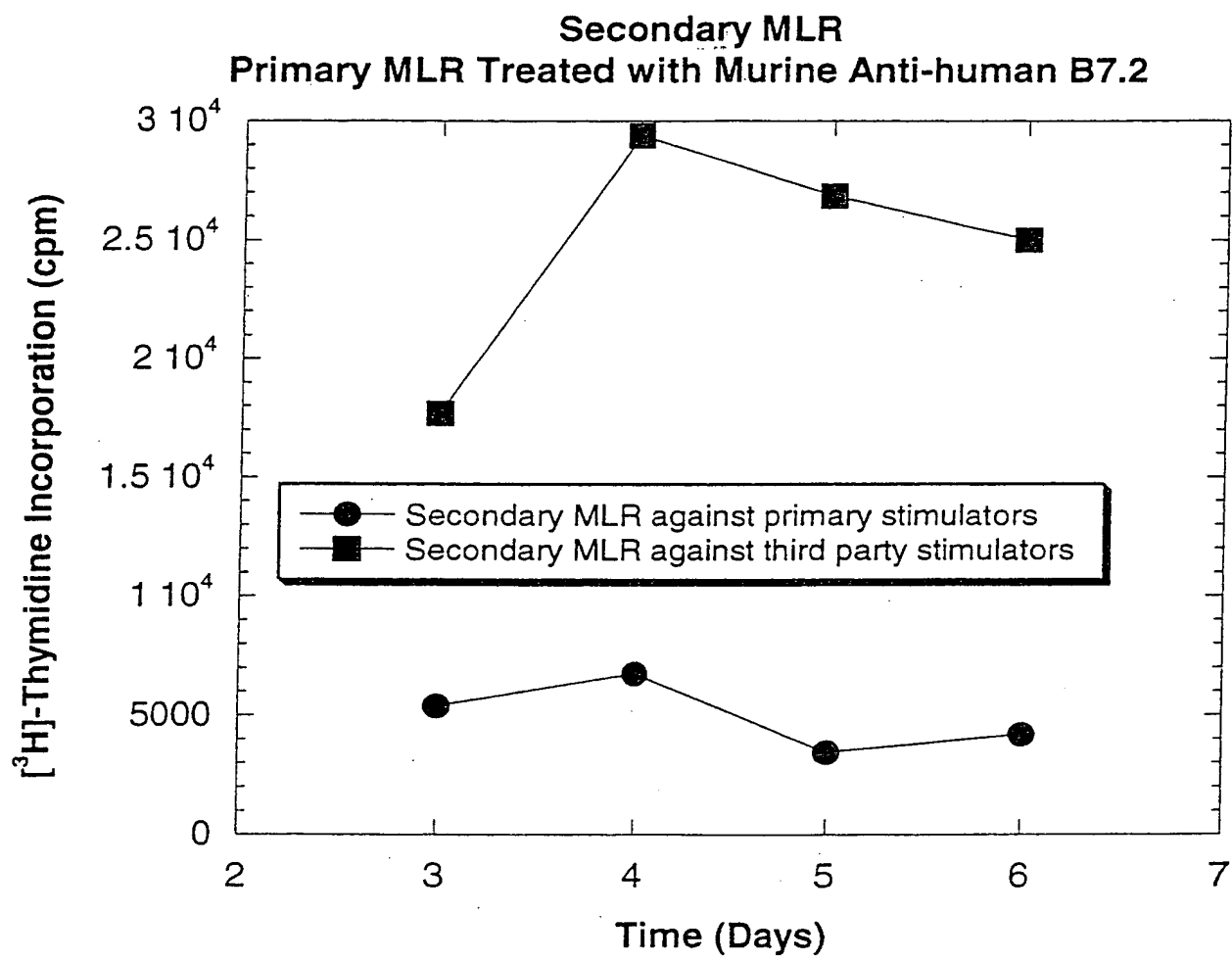


Figure 7

004240" 96842960

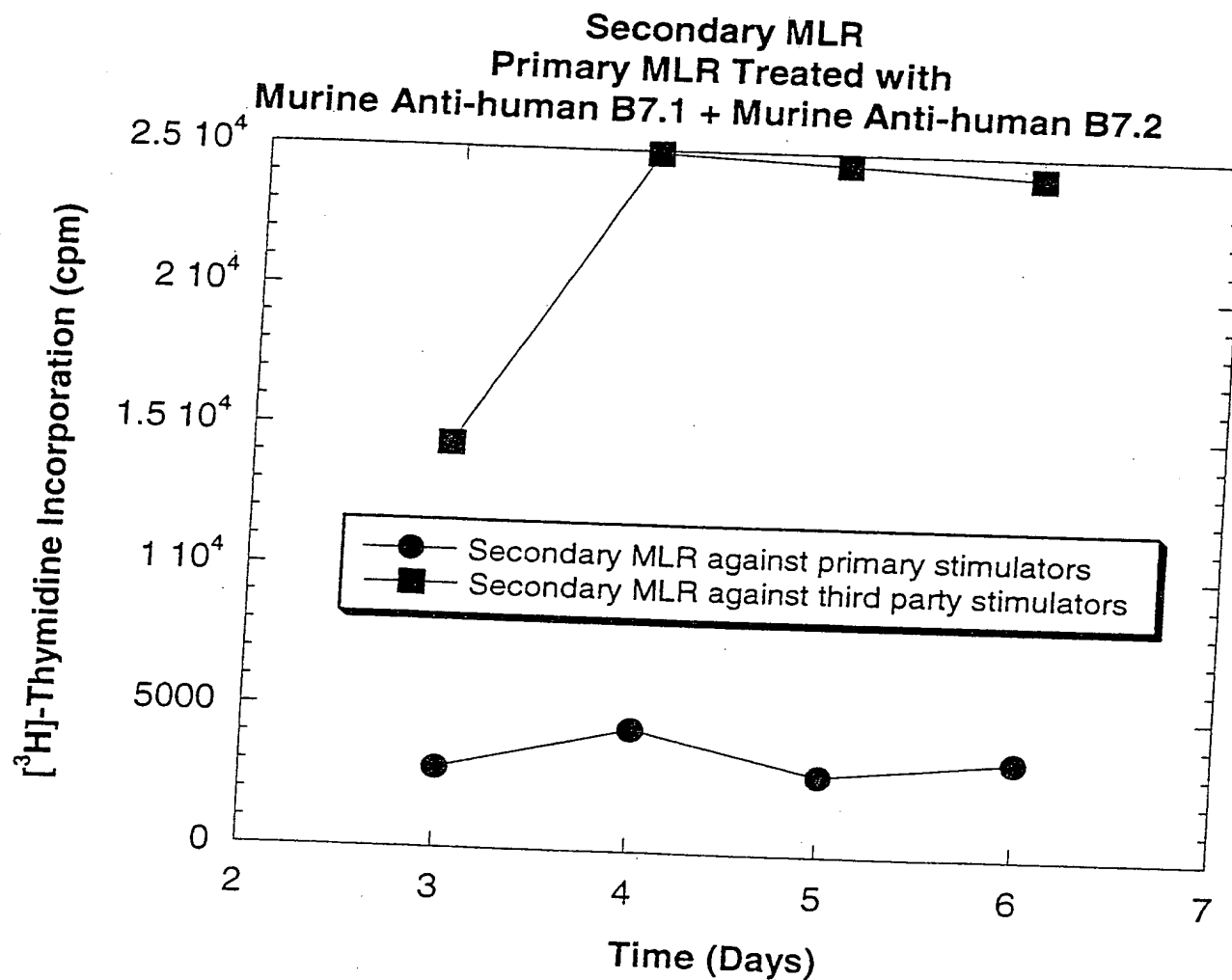
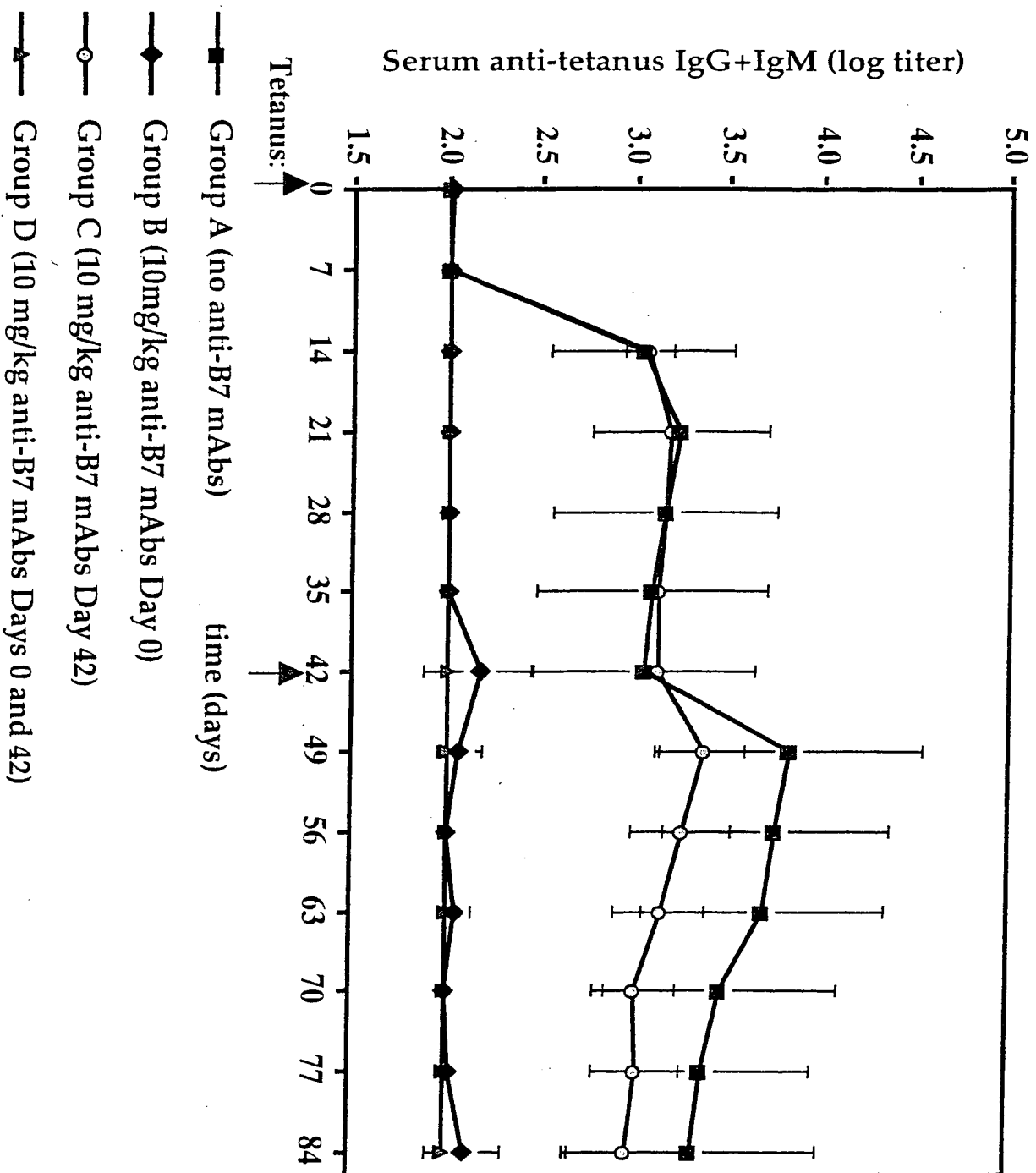


Figure 8

Antibody Response to Tetanus Immunization During Costimulation Blockade with Humanized Anti-B7.1 and Anti-B7.2



00/2/0" 968/2960

Anti-B7-2, Serum concentration
(ug/mL)

Serum Concentration of Humanized Anti-B7-2 in cynomolgus Monkeys

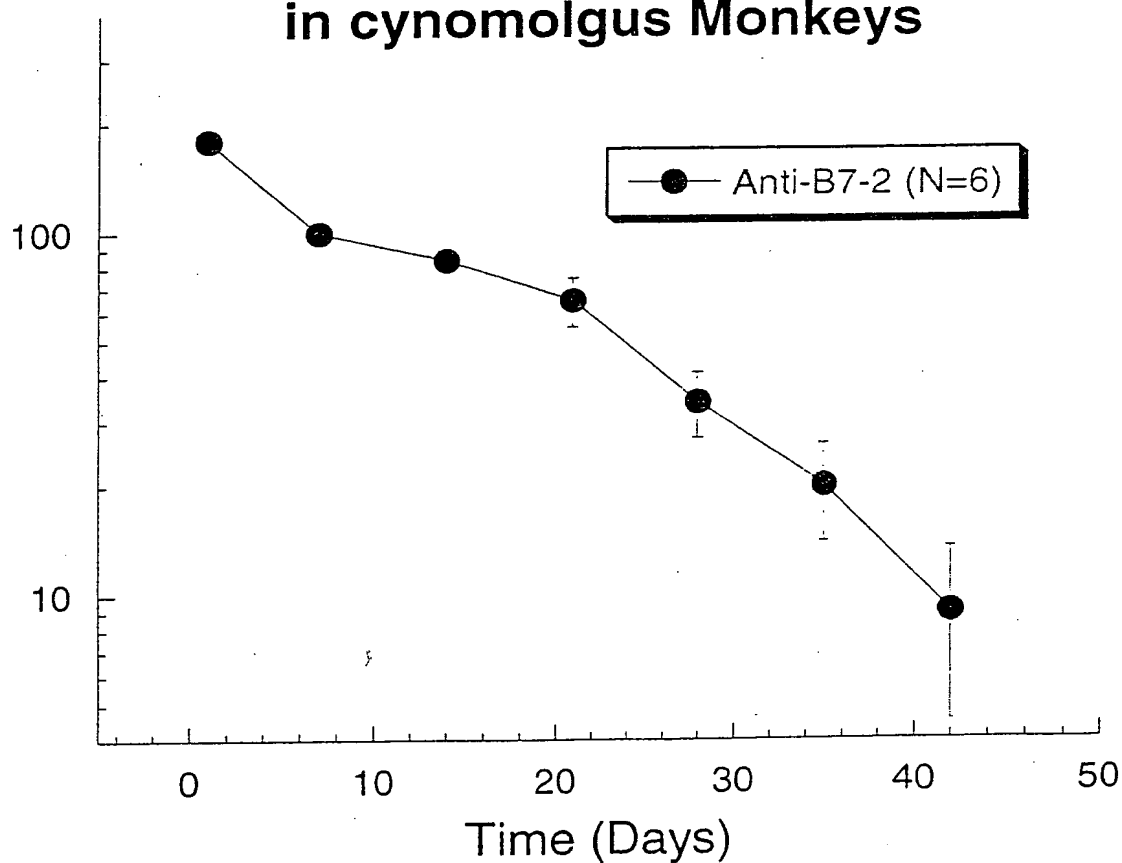


Figure 10